09/748,739

WEST Search History

DATE: Wednesday, January 29, 2003

Set Name side by side	Query	Hit Count	Set Name result set
	DB=USPT,PGPB,JPAB,EPAB,DWPI,TDBD; PLUR=YES; OP=OR		
L11	L10 not (l9 or l7 or l3)	22	L11
L10	(butyrylcholinesterase$ or bche).clm.	29	L10
L9	L8 not (l7 or l3)	25	L9
L8	(butyrylcholinesterase$ or bche) near3(peptide$ or variant$ or analog$)	30	L8
L7	(butyrylcholinesterase$ or bche) and l6	2	L7
L6	L5 or l4	302	L6
L5	(applied)near2(molecular)near2(evolution)	60	L5
L4	(board)near2(regents)near4(university)near2(nebraska)	242	L4
L3	L2 and l1	6	L3
L2	watkins	15292	L2
L1	lockridge	202	L1

END OF SEARCH HISTORY

09/748,739

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(FILE 'HOME' ENTERED AT 16:28:07 ON 29 JAN 2003)

     FILE 'REGISTRY' ENTERED AT 16:28:16 ON 29 JAN 2003
L1            26 S VTIICIRF/SQSP
L2            34 S ESCVGL/SQSP
L3            25 S L1 AND L2
L4            33 S DYTSKKESCVGL/SQSP
L5            25 S L1 AND L4

     FILE 'CAPLUS' ENTERED AT 16:30:07 ON 29 JAN 2003
L6             8 S L5

     FILE 'REGISTRY' ENTERED AT 16:35:49 ON 29 JAN 2003
L7            15 S ( 110737-66-1 OR 252323-27-6 OR 252323-33-4 OR 252323-35-6 OR

     FILE 'CAPLUS' ENTERED AT 16:37:42 ON 29 JAN 2003
L8             3 S L7

     FILE 'STNGUIDE' ENTERED AT 16:40:25 ON 29 JAN 2003

     FILE 'REGISTRY' ENTERED AT 16:44:35 ON 29 JAN 2003
L9             1 S 110737-66-1/RN
L10            1 S 108688-20-6/RN

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L6 ANSWER 1 OF 8 CAPLUS COPYRIGHT 2003 ACS

2002:637842 Document No. 137:181600 Butyrylcholinesterase variants with increased catalytic efficiency against cocaine and their analytical and therapeutic uses. Lockridge, Oksana; Watkins, Jeffry D.; Pancook, James D. (Applied Molecular Evolution, Inc., USA; University of Nebraska Medical Center). PCT Int. Appl. WO 2002064796 A2 20020822, 150 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN: PIXXD2. APPLICATION: WO 2001-US50450 20011221. PRIORITY: US 2000-748739 20001226; US 2001-32233 20011220.

AB The invention provides twenty-five butyrylcholinesterase variants having increased cocaine hydrolysis activity as well as the corresponding encoding nucleic acids. The invention also provides libraries of butyrylcholinesterase variants as well as libraries of the corresponding nucleic acids encoding butyrylcholinesterase variants. The invention further provides methods of hydrolyzing a cocaine-based butyrylcholinesterase substrate as well as methods of treating a cocaine-induced condition. Variants showing rates of cocaine hydrolysis that are 1.5-100-fold higher than that of the wild-type human enzyme are described. Guidelines for optimization of catalytic activity and the design of new variants are also disclosed.

IT **449829-16-7**

RL: PRP (Properties)

(unclaimed sequence; butyrylcholinesterase variants with increased catalytic efficiency against cocaine and their anal. and therapeutic uses)

L6 ANSWER 2 OF 8 CAPLUS COPYRIGHT 2003 ACS

1999:811389 Document No. 132:59182 Use of BCHE genotype in the prediction of whether cholinomimetic or non-cholinomimetic therapies will help a patient in the treatment of a neurological disease. Sevigny, Pierre; Wiebusch, Heiko; Schappert, Keith (Nova Molecular, Inc., Can.). PCT Int. Appl. WO 9966072 A2 19991223, 37 pp. DESIGNATED STATES: W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG. (English). CODEN: PIXXD2. APPLICATION: WO 1999-IB1298 19990616. PRIORITY: US 1998-89406 19980616.

AB The invention provides for the use of the polymorphic gene variant BCHE-K, which encodes a human butyrylcholinesterase with reduced catalytic activity, in predicting whether cholinomimetic or non-cholinomimetic therapies will help a patient in the treatment of a neurol. disease. Detn. of the patient's BCHE-K allele status as being heterozygous or homozygous is predictive of the patient having a poor response to a therapy for a neurol. disease. In preferred embodiments, the prediction of drug efficacy involves cholinomimetic therapies, preferably tacrine, or non-cholinomimetic therapies, preferably a vasopressinergic drug.

IT **252967-21-8**

RL: ARU (Analytical role, unclassified); BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); OCCU (Occurrence); USES (Uses)

(amino acid sequence; use of BCHE genotype in the prediction of whether cholinomimetic or non-cholinomimetic therapies will help a patient in the treatment of a neurol. disease)

IT **110737-66-1**
RL: ARU (Analytical role, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(amino acid sequence; use of BCHE genotype in the prediction of whether cholinomimetic or non-cholinomimetic therapies will help a patient in the treatment of a neurol. disease)

L6 ANSWER 3 OF 8 CAPLUS COPYRIGHT 2003 ACS
1999:794264 Document No. 132:32680 Esterase mutants for detoxification of organophosphates. Broomfield, Clarence A.; Millard, Charles B.; Lockridge, Oksana (United States Dept. of the Army, USA). U.S. US 6001625 A 19991214, 64 pp. (English). CODEN: USXXAM. APPLICATION: US 1995-446100 19950519.

AB A method of modifying esterases by substitution with histidine of at least one amino acid within 6 .ANG. of an active site serine provides esterases useful for detoxifying organophosphates. Thus, G117H human butyrylcholinesterase was produced. This mutant enzyme catalyzed the hydrolysis of VX at 25.degree. and pH 7.5 with turnover no. of 5 X 10-4 sec-1, a 350-fold increase over spontaneous hydrolysis under the same conditions. This enzyme was also able to hydrolyze sarin, DFP, methylphosphonothioate, and Echothiophate.

IT **110737-66-1 252323-27-6 252323-33-4 252323-35-6 252323-37-8 252323-42-5 252323-44-7 252323-47-0 252323-72-1 252323-73-2 252323-77-6 252323-78-7 252323-81-2 252323-83-4 252323-84-5**
RL: PRP (Properties)
(unclaimed protein sequence; esterase mutants for detoxification of organophosphates)

L6 ANSWER 4 OF 8 CAPLUS COPYRIGHT 2003 ACS
1994:673417 Document No. 121:273417 Promoter and transcription start site of human and rabbit butyrylcholinesterase genes. Jbilo, Omar; Toutant, Jean-Pierre; Vatsis, Kostas P.; Chatonnet, Arnaud; Lockridge, Oksana (Inst. Natl. Recherche Agronomique, Montpellier, 34060, Fr.). Journal of Biological Chemistry, 269(33), 20829-37 (English) 1994. CODEN: JBCHA3. ISSN: 0021-9258.

AB Two kilobase segments of the 5'-untranslated regions of the human and rabbit butyrylcholinesterase (BCHE) genes were characterized. The sequences shared extensive identity except for a 333-base pair (bp) Alu repeat present only in human BCHE. One single transcription start site was found in both genes with the techniques of primer extension, amplification of the 5'-end of mRNA, and RNase protection. Cap sites in human and rabbit BCHE genes were found in strictly homologous positions. In human BCHE, the transcription start site was found 157 bp upstream of Met-28, the translation start site. Potential regulatory elements in both promoters included one AP1 site and multiple sites for topoisomerase, Oct-1 and PEA-3. Transient expression of BCHE-reporter gene constructs showed that a 194-bp fragment of the 5'-flanking region of human BCHE and a 570-bp fragment of rabbit BCHE were sufficient for promoting chloramphenicol acetyltransferase activity in HeLa cells. No consensus TATA and CAAT boxes were found. However, the sequence around the transcription start site exhibited homol. with initiator elements found in other TATA-less promoters in developmentally regulated genes.

IT **158028-75-2**
RL: PRP (Properties)
(amino acid sequence of)

L6 ANSWER 5 OF 8 CAPLUS COPYRIGHT 2003 ACS
1990:31437 Document No. 112:31437 Structure of the gene for human butyrylcholinesterase. Evidence for a single copy. Arpagaus, Martine; Kott, Matthew; Vatsis, Kostas P.; Bartels, Cynthia F.; La Du, Bert N.; Lockridge, Oksana (Med. Sch., Univ. Michigan, Ann Abor, MI, 48109-0626, USA). Biochemistry, 29(1), 124-31 (English) 1990. CODEN: BICHAW. ISSN: 0006-2960.

AB Five genomic clones for human butyrylcholinesterase (BChE) were isolated using cDNA probes encoding the catalytic subunit of the hydrophilic tetramer. The BChE gene is .gtoreq.73 kb long and contains 4 exons. Exon 1 contains untranslated sequences and 2 potential translation initiation sites at codons -69 and -47. Exon 2 (1525 bp) contains 83% of the coding sequence for the mature protein, including the N-terminal and the active-site serine, and a third possible translation initiation site (likely functional) at codon -28. Exon 3 is 167 nucleotides long. Exon 4 (604 bp) codes for the C-terminus of the protein and the 3' untranslated region where 2 polyadenylation signals were identified. Intron 1 is 6.5 kb long, and the minimal sizes of introns 2 and 3 are each 32 kb. Southern blot anal. of total human genomic DNA is in complete agreement with the gene structure established by restriction endonuclease mapping of the genomic clones; this strongly suggests that the BChE gene is present in a single copy.

IT **123962-88-9**
RL: PRP (Properties)
(amino acid sequence of)

L6 ANSWER 6 OF 8 CAPLUS COPYRIGHT 2003 ACS
1988:467894 Document No. 109:67894 Brain cDNA clone for human cholinesterase. McTiernan, Charles; Adkins, Steve; Chatonnet, Arnaud; Vaughan, Theresa A.; Bartels, Cynthia F.; Kott, Matthew; Rosenberry, Terrone L.; La Du, Bert N.; Lockridge, Oksana (Sch. Med., Case West. Reserve Univ., Cleveland, OH, 44106, USA). Proceedings of the National Academy of Sciences of the United States of America, 84(19), 6682-6 (English) 1987. CODEN: PNASA6. ISSN: 0027-8424.

AB A cDNA library from human basal ganglia was screened with oligonucleotide probes corresponding to portions of the amino acid sequence of human serum cholinesterase (EC 3.1.1.8). Five overlapping clones, representing 2.4 kilobases, were isolated. The sequenced cDNA contained 207 base pairs of coding sequence 5' to the amino terminus of the mature protein in which there were four ATG translation start sites in the same reading frame as the protein. Only the ATG coding for Met-(-28) lay within a favorable consensus sequence for functional initiators. There were 1722 base pairs of coding sequence corresponding to the protein found circulating in human serum. The amino acid sequence deduced from the cDNA exactly matched the 574 amino acid sequence of human serum cholinesterase, as previously detd. by Edman degrdn. Therefore, these clones represented cholinesterase (EC 3.1.1.8) rather than acetylcholinesterase (EC 3.1.1.7). It was concluded that the amino acid sequences of cholinesterase from 2 different tissues, human brain and human serum, were identical. Hybridization of genomic DNA blots suggested that a single gene, or very few genes, coded for cholinesterase.

IT **112845-46-2**
RL: PRP (Properties)
(amino acid sequence of)

L6 ANSWER 7 OF 8 CAPLUS COPYRIGHT 2003 ACS
1987:569764 Document No. 107:169764 Isolation and characterization of full-length cDNA clones coding for cholinesterase from fetal human tissues. Prody, Catherine A.; Zevin-Sonkin, Dina; Gnatt, Averell; Goldberg, Ora; Soreq, Hermona (Dep. Neurobiol., Weizmann Inst. Sci., Rehovot, 76100, Israel). Proceedings of the National Academy of Sciences of the United States of America, 84(11), 3555-9 (English) 1987. CODEN:

PNASA6. ISSN: 0027-8424.

AB To study the primary structure and regulation of human cholinesterases, oligodeoxynucleotide probes were prepd. according to a consensus peptide sequence present in the active site of both human serum butyrylcholinesterase (BtChoEase; EC 3.1.1.8) and Torpedo elec. organ true acetylcholinesterase (AcChoEase; EC 3.1.1.7). Using these probes several cDNA clones were isolated from phage .lambda.gt10 libraries of fetal brain and liver origins. These include 2.4-kilobase cDNA clones that code for a polypeptide contg. a putative signal peptide and the N-terminal, active site, and C-terminal peptides of human BtChoEase, suggesting the they code either for BtChoEase itself or for a very similar but distinct fetal form of cholinesterase. In RNA blots of poly(A)+ RNA from the cholinesterase-producing fetal brain and liver, these cDNAs hybridized with a single 2.5-kilobase band. Blot hybridization to human genomic DNA revealed that these fetal BtChoEase cDNA clones hybridize with DNA fragments of the total length of 17.5 kilobases, and signal intensities indicated that these sequences are not present in many copies. Both the cDNA-encoded protein and its nucleotide sequence display striking homol. to parallel sequences published for Torpedo AcChoEase. These findings demonstrate extensive homologies between the fetal BtChoEase encoded by these clones and other cholinesterases of various forms and species.

IT **110737-66-1**
RL: PRP (Properties)
(amino acid sequence of)

L6 ANSWER 8 OF 8 CAPLUS COPYRIGHT 2003 ACS

1987:401975 Document No. 107:1975 Human cholinesterase-type proteins. Soreq, Hermona (Yeda Research and Development Co. Ltd., Israel). Eur. Pat. Appl. EP 206200 A2 19861230, 44 pp. DESIGNATED STATES: R: AT, BE, CH, DE, FR, GB, IT, LI, LU, NL, SE. (English). CODEN: EPXXDW. APPLICATION: EP 1986-108189 19860616. PRIORITY: IL 1985-75553 19850618.

AB The cDNA for a human acetylcholinesterase is isolated and sequenced. A fragment encoding part of the cholinesterase is cloned and expressed as a fusion protein with .beta.-galactosidase. Antibodies to the fusion protein are produced. A cDNA library was constructed from total mRNA of human fetal brain, and was screened by hybridization with oligonucleotide probes encoding (1) a hexapeptide consensus sequence from the organophosphate-binding site of cholinesterases, and (2) the hexapeptide sequence plus an addnl. 4 amino acids corresponding to the sequence of a human serum pseudocholinesterase. A 40-kilodalton recombinant polypeptide interacted in protein blots with antibodies to human erythrocyte and Torpedo elec. organ acetylcholinesterase. Antibodies to the recombinant protein were immunoreactive with human acetylcholinesterase and pseudocholinesterase.

IT **108688-20-6**
RL: PRP (Properties)
(amino acid sequence of)

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L8 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2003 ACS

1999:811389 Document No. 132:59182 Use of BCHE genotype in the prediction of whether cholinomimetic or non-cholinomimetic therapies will help a patient in the treatment of a neurological disease. Sevigny, Pierre; Wiebusch, Heiko; Schappert, Keith (Nova Molecular, Inc., Can.). PCT Int. Appl. WO 9966072 A2 19991223, 37 pp. DESIGNATED STATES: W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG. (English). CODEN: PIXXD2. APPLICATION: WO 1999-IB1298 19990616. PRIORITY: US 1998-89406 19980616.

AB The invention provides for the use of the polymorphic gene variant BCHE-K, which encodes a human butyrylcholinesterase with reduced catalytic activity, in predicting whether cholinomimetic or non-cholinomimetic therapies will help a patient in the treatment of a neurol. disease. Detn. of the patient's BCHE-K allele status as being heterozygous or homozygous is predictive of the patient having a poor response to a therapy for a neurol. disease. In preferred embodiments, the prediction of drug efficacy involves cholinomimetic therapies, preferably tacrine, or non-cholinomimetic therapies, preferably a vasopressinergic drug.

IT **110737-66-1**

RL: ARU (Analytical role, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)

(amino acid sequence; use of BCHE genotype in the prediction of whether cholinomimetic or non-cholinomimetic therapies will help a patient in the treatment of a neurol. disease)

L8 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2003 ACS

1987:569764 Document No. 107:169764 Isolation and characterization of full-length cDNA clones coding for cholinesterase from fetal human tissues. Prody, Catherine A.; Zevin-Sonkin, Dina; Gnatt, Averell; Goldberg, Ora; Soreq, Hermona (Dep. Neurobiol., Weizmann Inst. Sci., Rehovot, 76100, Israel). Proceedings of the National Academy of Sciences of the United States of America, 84(11), 3555-9 (English) 1987. CODEN: PNASA6. ISSN: 0027-8424.

AB To study the primary structure and regulation of human cholinesterases, oligodeoxynucleotide probes were prepd. according to a consensus peptide sequence present in the active site of both human serum butyrylcholinesterase (BtChoEase; EC 3.1.1.8) and Torpedo elec. organ true acetylcholinesterase (AcChoEase; EC 3.1.1.7). Using these probes several cDNA clones were isolated from phage .lambda.gt10 libraries of fetal brain and liver origins. These include 2.4-kilobase cDNA clones that code for a polypeptide contg. a putative signal peptide and the N-terminal, active site, and C-terminal peptides of human BtChoEase, suggesting the they code either for BtChoEase itself or for a very similar but distinct fetal form of cholinesterase. In RNA blots of poly(A)+ RNA from the cholinesterase-producing fetal brain and liver, these cDNAs hybridized with a single 2.5-kilobase band. Blot hybridization to human genomic DNA revealed that these fetal BtChoEase cDNA clones hybridize with DNA fragments of the total length of 17.5 kilobases, and signal intensities indicated that these sequences are not present in many copies. Both the cDNA-encoded protein and its nucleotide sequence display striking homol. to parallel sequences published for Torpedo AcChoEase. These findings demonstrate extensive homologies between the fetal BtChoEase encoded by these clones and other cholinesterases of various forms and species.

IT **110737-66-1**

RL: PRP (Properties)

(amino acid sequence of)

L6 ANSWER 8 OF 8 CAPLUS COPYRIGHT 2003 ACS

1987:401975 Document No. 107:1975 Human cholinesterase-type proteins. Soreq, Hermona (Yeda Research and Development Co. Ltd., Israel). Eur. Pat. Appl. EP 206200 A2 19861230, 44 pp. DESIGNATED STATES: R: AT, BE, CH, DE, FR, GB, IT, LI, LU, NL, SE. (English). CODEN: EPXXDW. APPLICATION: EP 1986-108189 19860616. PRIORITY: IL 1985-75553 19850618.

AB The cDNA for a human acetylcholinesterase is isolated and sequenced. A fragment encoding part of the cholinesterase is cloned and expressed as a fusion protein with .beta.-galactosidase. Antibodies to the fusion protein are produced. A cDNA library was constructed from total mRNA of human fetal brain, and was screened by hybridization with oligonucleotide probes encoding (1) a hexapeptide consensus sequence from the organophosphate-binding site of cholinesterases, and (2) the hexapeptide sequence plus an addnl. 4 amino acids corresponding to the sequence of a human serum pseudocholinesterase. A 40-kilodalton recombinant polypeptide interacted in protein blots with antibodies to human erythrocyte and Torpedo elec. organ acetylcholinesterase. Antibodies to the recombinant protein were immunoreactive with human acetylcholinesterase and pseudocholinesterase.

IT **108688-20-6**

RL: PRP (Properties)

(amino acid sequence of)

L9 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2003 ACS
RN **110737-66-1** REGISTRY
CN Esterase, choline (human clone FL39 precursor protein moiety reduced) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 22: PN: US6001625 SEQID: 1 unclaimed protein
CN 2: PN: WO9966072 SEQID: 3 claimed protein
CN Esterase, choline (human gene BCHE)
FS PROTEIN SEQUENCE
MF Unspecified
CI MAN
SR CA
LC STN Files: CA, CAPLUS, TOXCENTER, USPATFULL

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
*** USE 'SQD' OR 'SQIDE' FORMATS TO DISPLAY SEQUENCE ***
3 REFERENCES IN FILE CA (1962 TO DATE)
3 REFERENCES IN FILE CAPLUS (1962 TO DATE)

=> d seq3

L9 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2003 ACS

SEQ3
1 Met-His-Ser-Lys-Val-Thr-Ile-Ile-Cys-Ile-
11 Arg-Phe-Leu-Phe-Trp-Phe-Leu-Leu-Leu-Cys-
21 Met-Leu-Ile-Gly-Lys-Ser-His-Thr-Glu-Asp-
31 Asp-Ile-Ile-Ile-Ala-Thr-Lys-Asn-Gly-Lys-
41 Val-Arg-Gly-Met-Asn-Leu-Thr-Val-Phe-Gly-
51 Gly-Thr-Val-Thr-Ala-Phe-Leu-Gly-Ile-Pro-
61 Tyr-Ala-Gln-Pro-Pro-Leu-Gly-Arg-Leu-Arg-
71 Phe-Lys-Lys-Pro-Gln-Ser-Leu-Thr-Lys-Trp-
81 Ser-Asp-Ile-Trp-Asn-Ala-Thr-Lys-Tyr-Ala-
91 Asn-Ser-Cys-Cys-Gln-Asn-Ile-Asp-Gln-Ser-
101 Phe-Pro-Gly-Phe-His-Gly-Ser-Glu-Met-Trp-
111 Asn-Pro-Asn-Thr-Asp-Leu-Ser-Glu-Asp-Cys-
121 Leu-Tyr-Leu-Asn-Val-Trp-Ile-Pro-Ala-Pro-
131 Lys-Pro-Lys-Asn-Ala-Thr-Val-Leu-Ile-Trp-
141 Ile-Tyr-Gly-Gly-Gly-Phe-Gln-Thr-Gly-Thr-
151 Ser-Ser-Leu-His-Val-Tyr-Asp-Gly-Lys-Phe-
161 Leu-Ala-Arg-Val-Glu-Arg-Val-Ile-Val-Val-
171 Ser-Met-Asn-Tyr-Arg-Val-Gly-Ala-Leu-Gly-
181 Phe-Leu-Ala-Leu-Pro-Gly-Asn-Pro-Glu-Ala-
191 Pro-Gly-Asn-Met-Gly-Leu-Phe-Asp-Gln-Gln-
201 Leu-Ala-Leu-Gln-Trp-Val-Gln-Lys-Asn-Ile-
211 Ala-Ala-Phe-Gly-Gly-Asn-Pro-Lys-Ser-Val-
221 Thr-Leu-Phe-Gly-Glu-Ser-Ala-Gly-Ala-Ala-
231 Ser-Val-Ser-Leu-His-Leu-Leu-Ser-Pro-Gly-
241 Ser-His-Ser-Leu-Phe-Thr-Arg-Ala-Ile-Leu-
251 Gln-Ser-Gly-Ser-Phe-Asn-Ala-Pro-Trp-Ala-
261 Val-Thr-Ser-Leu-Tyr-Glu-Ala-Arg-Asn-Arg-
271 Thr-Leu-Asn-Leu-Ala-Lys-Leu-Thr-Gly-Cys-
281 Ser-Arg-Glu-Asn-Glu-Thr-Glu-Ile-Ile-Lys-
291 Cys-Leu-Arg-Asn-Lys-Asp-Pro-Gln-Glu-Ile-
301 Leu-Leu-Asn-Glu-Ala-Phe-Val-Val-Pro-Tyr-
311 Gly-Thr-Pro-Leu-Ser-Val-Asn-Phe-Gly-Pro-
321 Thr-Val-Asp-Gly-Asp-Phe-Leu-Thr-Asp-Met-
331 Pro-Asp-Ile-Leu-Leu-Glu-Leu-Gly-Gln-Phe-
341 Lys-Lys-Thr-Gln-Ile-Leu-Val-Gly-Val-Asn-
351 Lys-Asp-Glu-Gly-Thr-Ala-Phe-Leu-Val-Tyr-
361 Gly-Ala-Pro-Gly-Phe-Ser-Lys-Asp-Asn-Asn-

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371 Ser-Ile-Ile-Thr-Arg-Lys-Glu-Phe-Gln-Glu-
381 Gly-Leu-Lys-Ile-Phe-Phe-Pro-Gly-Val-Ser-
391 Glu-Phe-Gly-Lys-Glu-Ser-Ile-Leu-Phe-His-
401 Tyr-Thr-Asp-Trp-Val-Asp-Asp-Gln-Arg-Pro-
411 Glu-Asn-Tyr-Arg-Glu-Ala-Leu-Gly-Asp-Val-
421 Val-Gly-Asp-Tyr-Asn-Phe-Ile-Cys-Pro-Ala-
431 Leu-Glu-Phe-Thr-Lys-Lys-Phe-Ser-Glu-Trp-
441 Gly-Asn-Asn-Ala-Phe-Phe-Tyr-Tyr-Phe-Glu-
451 His-Arg-Ser-Ser-Lys-Leu-Pro-Trp-Pro-Glu-
461 Trp-Met-Gly-Val-Met-His-Gly-Tyr-Glu-Ile-
471 Glu-Phe-Val-Phe-Gly-Leu-Pro-Leu-Glu-Arg-
481 Arg-Asp-Asn-Tyr-Thr-Lys-Ala-Glu-Glu-Ile-
491 Leu-Ser-Arg-Ser-Ile-Val-Lys-Arg-Trp-Ala-
501 Asn-Phe-Ala-Lys-Tyr-Gly-Asn-Pro-Asn-Glu-
511 Thr-Gln-Asn-Asn-Ser-Thr-Ser-Trp-Pro-Val-
521 Phe-Lys-Ser-Thr-Glu-Gln-Lys-Tyr-Leu-Thr-
531 Leu-Asn-Thr-Glu-Ser-Thr-Arg-Ile-Met-Thr-
541 Lys-Leu-Arg-Ala-Gln-Gln-Cys-Arg-Phe-Trp-
551 Thr-Ser-Phe-Phe-Pro-Lys-Val-Leu-Glu-Met-
561 Thr-Gly-Asn-Ile-Asp-Glu-Ala-Glu-Trp-Glu-
571 Trp-Lys-Ala-Gly-Phe-His-Arg-Trp-Asn-Asn-
581 Tyr-Met-Met-Asp-Trp-Lys-Asn-Gln-Phe-Asn-
591 Asp-Tyr-Thr-Ser-Lys-Lys-Glu-Ser-Cys-Val-
601 Gly-Leu
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L10 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2003 ACS
RN **108688-20-6** REGISTRY
CN Esterase, acetyl choline (human clone FChE precursor reduced) (9CI) (CA INDEX NAME)
FS PROTEIN SEQUENCE
MF Unspecified
CI MAN
SR CA
LC STN Files: CA, CAPLUS, TOXCENTER, USPATFULL

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
*** USE 'SQD' OR 'SQIDE' FORMATS TO DISPLAY SEQUENCE ***
1 REFERENCES IN FILE CA (1962 TO DATE)
1 REFERENCES IN FILE CAPLUS (1962 TO DATE)

=> d seq3

L10 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2003 ACS

SEQ3
1 Met-His-Ser-Lys-Val-Thr-Ile-Ile-Cys-Ile-
11 Arg-Phe-Leu-Phe-Trp-Phe-Val-Leu-Leu-Cys-
21 Met-Leu-Ile-Gly-Lys-Ser-His-Thr-Glu-Asp-
31 Asp-Ile-Ile-Ile-Ala-Thr-Lys-Asn-Gly-Lys-
41 Val-Arg-Gly-Met-Asn-Leu-Thr-Val-Phe-Gly-
51 Gly-Thr-Val-Thr-Ala-Phe-Leu-Gly-Ile-Pro-
61 Tyr-Ala-Gln-Pro-Pro-Leu-Gly-Arg-Leu-Arg-
71 Phe-Thr-Lys-Pro-Gln-Ser-Leu-Thr-Arg-Trp-
81 Ser-Asp-Ile-Trp-Thr-Ala-Thr-Lys-Tyr-Ala-
91 Asn-Ser-Cys-Cys-Gln-Asn-Ile-Asp-His-Ser-
101 Phe-Pro-Gly-Phe-His-Gly-Ser-Glu-Met-Trp-
111 Asn-Pro-Asn-Thr-Asp-Leu-Ser-Glu-Asp-Cys-
121 Leu-Tyr-Leu-Asn-Val-Trp-Ile-Pro-Ala-Pro-
131 Lys-Pro-Lys-Asn-Ala-Thr-Val-Leu-Ile-Trp-
141 Ile-Tyr-Gly-Gly-Gly-Phe-Gln-Thr-Gly-Thr-
151 Ser-Ser-Leu-His-Val-Tyr-Asp-Gly-Lys-Phe-
161 Leu-Ala-Arg-Val-Glu-Arg-Val-Ile-Val-Val-
171 Ser-Met-Asn-Tyr-Arg-Val-Gly-Ala-Leu-Gly-
181 Phe-Leu-Ala-Leu-Pro-Gly-Asn-Pro-Glu-Ala-
191 Pro-Gly-Asn-Met-Gly-Leu-Phe-Asp-Gln-Gln-
201 Leu-Ala-Leu-Gln-Trp-Val-Gln-Lys-Asn-Ile-
211 Ala-Ala-Phe-Gly-Gly-Asn-Pro-Lys-Ser-Val-
221 Thr-Leu-Phe-Gly-Glu-Ser-Ala-Gly-Ala-Ala-
231 Ser-Val-Ser-Leu-His-Leu-Leu-Ser-Pro-Gly-
241 Ser-His-Ser-Leu-Phe-Thr-Arg-Ala-Ile-Leu-
251 Gln-Ser-Gly-Ser-Phe-Asn-Ala-Pro-Trp-Ala-
261 Val-Thr-Ser-Leu-Tyr-Glu-Ala-Arg-Asn-Arg-
271 Thr-Leu-Asn-Leu-Ala-Lys-Leu-Thr-Gly-Cys-
281 Ser-Arg-Glu-Asn-Glu-Thr-Glu-Ile-Ile-Lys-
291 Cys-Leu-Arg-Asn-Lys-Asp-Pro-Gln-Glu-Ile-
301 Leu-Leu-Asn-Glu-Ala-Phe-Val-Val-Pro-Tyr-
311 Gly-Thr-Pro-Leu-Ser-Val-Asn-Phe-Gly-Pro-
321 Thr-Val-Asp-Gly-Asp-Phe-Leu-Thr-Asp-Met-
331 Pro-Asp-Ile-Leu-Leu-Glu-Leu-Gly-Gln-Phe-
341 Lys-Lys-Thr-Gln-Ile-Leu-Val-Gly-Val-Asn-
351 Lys-Asp-Glu-Gly-Thr-Ala-Phe-Leu-Val-Tyr-
361 Gly-Ala-Pro-Gly-Phe-Ser-Lys-Asp-Asn-Ile-
371 Ser-Ile-Ile-Thr-Arg-Lys-Glu-Phe-Gln-Glu-
381 Gly-Leu-Lys-Ile-Phe-Phe-Pro-Gly-Val-Ser-
391 Glu-Phe-Gly-Lys-Glu-Ser-Ile-Leu-Phe-Gln-
401 Tyr-Thr-Asp-Trp-Val-Asp-Asp-Gln-Arg-Pro-

411 Glu-Asp-Tyr-Arg-Glu-Ala-Leu-Gly-Cys-Met-
421 Leu-Leu-Gly-Ile-Ile-Ile-Ser-Tyr-Ala-Leu-
431 Pro-Phe-Glu-Val-Thr-Lys-Lys-Phe-Ser-Glu-
441 Trp-Gly-Asn-Asn-Ala-Phe-Phe-Tyr-Tyr-Phe-
451 Glu-His-Arg-Ser-Ser-Lys-Leu-Pro-Trp-Pro-
461 Glu-Trp-Met-Gly-Val-Met-His-Gly-Tyr-Lys-
471 Leu-Asn-Leu-Ser-Leu-Val-Tyr-Leu-Trp-Lys-
481 Glu-Glu-Ile-Ile-Thr-Gln-Asn-Pro-Ile-Lys-
491 Phe-Lys-Tyr-Ile-His-Ser-Lys-Arg-Trp-Ala-
501 Asn-Phe-Ala-Lys-Tyr-Gly-Asn-Pro-Asn-Glu-
511 Thr-Gln-Thr-Ile-Ser-Thr-Ser-Trp-Pro-Val-
521 Leu-Lys-Ala-Leu-Asn-Lys-Ile-Ser-Asn-Leu-
531 Glu-Tyr-Arg-Val-Asn-Lys-Asn-Asn-Asp-Glu-
541 Thr-Thr-Cys-Ser-Thr-Met-Ser-Ile-Leu-Asp-
551 Ile-Ile-Phe-Ser-Lys-Ser-Leu-Gly-Asn-Asp-
561 Arg-Lys-Tyr-Asp-Glu-Ala-Glu-Trp-Glu-Trp-
571 Lys-Ala-Gly-Phe-His-Arg-Trp-Asn-Asn-Tyr-
581 Met-Met-Asp-Trp-Lys-Asn-Gln-Phe-Asn-Asp-
591 Tyr-Thr-Ser-Lys-Lys-Glu-Ser-Cys-Val-Gly-
601 Leu

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